Specification

Please amend paragraphs of the published application, i.e. U.S. Published Patent Application No. 20050250101 A1, [0098], [0101], [0107], [0108], [0111] – [0114], [0117] – [0119], and [0121] – [0123] as follows:

[0098] The procedure of PCR and base sequencing of the oligonucleotides was as the following. The sequence of the oligonucleotide composed of 40 base pairs (40 mer) was 5'-agc att ttg tgg ggc gtg ata gcc tcc ttg gcc gca aag a-3' (SEQ ID NO 1), and in PCR, forward primer sequence was 5'-agc att ttg tgg ggc-3' (15 mer, SEQ ID NO. 2), reverse primer sequence was 5'-cc ttg gcc gca aag acc acc acc tcg cgg-3' (29 mer, SEQ ID NO 3)[-3']. To increase the efficiency of PCR, reverse primer was set as 29 base pairs (29 mer), not 15 base pairs (15 mer). To analyze base sequence of oligonucleotides which had been amplified by PCR, the amplified oligonucleotides were purified with DNA PrepMate II (DNA PrepMate II, product of Bioneer Corporation), and then, their base sequence was analyzed by direct base sequencing on 10% polyacrylamide gel. FIG. 4a and FIG. 4b present the results. FIG. 4a represents the results of agarose gel electrophoresis of the products obtained by the above procedure. From FIG. 4a, it is confirmed that oligonucleotide is recovered normally in the present invention. FIG. 4b represents the result of base sequencing of the amplified product of FIG. 4a. FIG. 4b shows that the sequence of original oligonucleotides and the sequence of amplified oligonucleotides coincided. Particularly, excluding the forward and reverse primer binding regions, the base sequence of code sequence region composed of 10 base pairs (gtg ata gcc t) coincided. Therefore, it was verified that forward primer and reverse primer recovered normally in the present invention. Therefore, it was verified that oligonucleotide could function as a marker by making each marker have different code sequence.

[0101] resulting base sequence: 5'-g ata gcc tcc ttg gcc gca aag acc acc acc-3' (SEQ ID NO 4)

[0107] resulted base sequence: 5'-ggt ggt ctt tgc ggc caa gga ggc tat cac gcc cca caa aat gct-3' (reverse cloned, SEQ ID NO 5)

[0108] analyzed base sequence: 5'-agc att ttg tgg ggc gtg ata gcc tcc ttg gcc gca aag acc acc-3' (SEQ ID 6)

[0111] expected base sequence : 5'-agc att ttg tgg ggc tgc ctg gcg ccc ttg gcc gca aag acc acc acc tcg cgg-3'(SEQ ID NO 7)

[0112] resulted base sequence of lane 1(A): 5'-agc att ttg tgg ggc tgc ctg gcg ccc ttg gcc gca aag acc acc acc tcg c-3' (SEQ ID NO 8)

[0113] resulted base sequence of lane 3(B): 5'-agc att ttg tgg ggc tgc ctg gcg gcc cac aaa atc gt-3' (SEQ ID NO 9)

[0114] The agarose gel electrophoresis was carried out to purify the amplified product of binding complex A by PCR, which was recovered from the mixture with vehicle coating paint. The results showed that the band was not formed well in the gel, and was not cloned into T-vector. In the present example, the sequence of forward primer for PCR was agc att ttg tgg ggc (SEQ ID NO 10). The next 10 sequence (tgc ctg gcg c, SEQ ID NO 11) was the sequence which functioned as a marker and it was confirmed that the base sequence coincided exactly. The sequence of reverse primer was 5'-cc ttg gcc gca aag acc acc acc tcg cgg-3' (29 mer). For binding complex A, the result was different according to the type of paint. When

mixed with urethane paint it was well recovered, so its base sequence was analyzed well. However, when mixed with vehicle coating paint, its base sequence analysis was failed because it was not cloned as it should be. These results showed that bases of the oligonucleotides reacted with vehicle coating paint directly and it resulted in poor recovery since protecting reaction for amino groups or oxygen atoms was not carried out.

[0117] Oligo sequence 1: ctg atg ggc cgc aac ctt cag tac att ttg ggc gca cca t (SEQ ID NO 12)

[0118] Oligo sequence 2: tca ttc ccc gac cgg agc agt cga tgg cgt ttc acc ggg t (SEQ ID NO 13)

[0119] Oligo sequence 3: cgc gcg gtg ttg aat tca tgg cca gtg gaa cgc ttt ccg c (SEQ ID NO 14)

[0121] primer 1 (forward: ctg atg ggc cgc aac (SEQ ID NO 15), reverse: atg gtg cgc cca aaa, (SEQ ID NO 16))

[0122] primer 2 (forward: tca ttc ccc gac cgg, reverse: acc cgg tga aac gcc (SEQ ID NO 18))

[0123] primer 3 (forward: cgc gcg gtg ttg aat, reverse: gcg gaa agc gtt cca (SEQ ID NO 20))

In the Figures

Figure 1 has been amended to clarify the subject matter described therein. Attached to this response is a Proposed Amendment to Figure 1 with marked up and a "Replacement Sheet" representing a clean copy of amended Figure 1.

Sequence Listing

Attached hereto are a sequence listing and a sequence listing submission statement, as well as a computer readable format copy of the sequence listing.